

## SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Symbicom AB  
(B) STREET: Tvistevägen 48  
(C) CITY: Umeå  
(E) COUNTRY: Sweden  
(F) POSTAL CODE (ZIP): S-907 36

## (ii) TITLE OF INVENTION: Pl3 antigens from Borrelia

(iii) NUMBER OF SEQUENCES: 31

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*  
(B) STRAIN: B313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Thr	Ser	Lys	Gln	Asp	Pro	Ile	Val	Pro	Phe	Leu	Leu	Asn	Leu	Phe	Leu
1				5					10					15	

Gly Phe Gly Ile Gly Ser Phe Ala Gln  
20 25

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

[illegible]

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ACNTCNAARC ARGAYCCNAT

20

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGNGCRAARC TNCCDATNCC

20

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 74 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACATCTAAGC AGGACCCTAT TGTACCATCT TTATTGAACC TTTTTTTAGG GTTTGGCATC

60

GGGAGCTTCG CCCA

74

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

09508497.031000

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGTACCATCT TTATTGAACC TTTTTTTAGG GTTT

34

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AAACCCTAAA AAAAGGTTCA ATAAAG

26

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GATTTTTCAT TGGATCCCAG AATTG

26

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

09508487 031000

26

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

21

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

31

(i) SEQUENCE CHARACTERISTICS:

700503

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGAATTCCTT GGTTCGCGT GGATCCATGA ATAACTTTT AATTTTGT

50

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TAAAAAATT TAAAGAAAAG GAGGG

25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGCTTATAGA ATCCGGGGCT TATTTGG

27

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

09508497 031000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TAGAATTCAG CAATTGCAAT ACAG

24

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CACCCATTTT CTAGATAAAT AAAATTAATA GC

32

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATAAAAGGTA CCATAGCTTT TTTTGAAAGA CAG

33

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

050487 031000

(A) ORGANISM: *Borrelia burgdorferi*  
 (B) STRAIN: B31

## (ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION:170..709

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

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ATTGTTAAAA GAATTGAAAT TGATAATTTT ATGGTCAAAT CAAGAAGCTC TATTGGGAAG      60
CGAATTTCAA GCAATAATTT GAAAAAAGTT AAATTTAAAT AACTTTAAAA ACCTTTTTTTA      120
AATTTCATTA ATATGCTACC ATAGTACCAG TTTTAATAAA GGGGTTTTTT ATG AAT      175
                                         Met Asn
                                         1

AAA CTT TTA ATT TTT GTT TTG GCA ACC TTT TGT GTT TTT TCT AGC TTT      223
Lys Leu Leu Ile Phe Val Leu Ala Thr Phe Cys Val Phe Ser Ser Phe
      5              10              15

GCT CAA GCT AAT GAT TCT AAA AAT GGT GCG TTT GGG ATG AGT GCT GGA      271
Ala Gln Ala Asn Asp Ser Lys Asn Gly Ala Phe Gly Met Ser Ala Gly
      20              25              30

GAA AAA CTT TTG GTT TAT GAA ACT AGC AAG CAA GAT CCT ATT GTA CCA      319
Glu Lys Leu Leu Val Tyr Glu Thr Ser Lys Gln Asp Pro Ile Val Pro
      35              40              45              50

TTT TTA TTG AAC CTT TTT TTA GGG TTT GGA ATA GGC TCC TTT GCT CAA      367
Phe Leu Leu Asn Leu Phe Leu Gly Phe Gly Ile Gly Ser Phe Ala Gln
      55              60              65

GGA GAT ATT CTT GGA GGT TCT CTT ATT CTT GGA TTT GAT GCG GTT GGT      415
Gly Asp Ile Leu Gly Gly Ser Leu Ile Leu Gly Phe Asp Ala Val Gly
      70              75              80

ATA GGG CTT ATA CTT GCG GGG GCT TAT TTG GAT ATC AAA GCG CTT GAT      463
Ile Gly Leu Ile Leu Ala Gly Ala Tyr Leu Asp Ile Lys Ala Leu Asp
      85              90              95

GGT ATT ACT AAA AAA GCT GCT TTT CAA TGG ACT TGG GGT AAG GGA GTT      511
Gly Ile Thr Lys Lys Ala Ala Phe Gln Trp Thr Trp Gly Lys Gly Val

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09503497 631000

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

Met Asn Lys Leu Leu Ile Phe Val Leu Ala Thr Phe Cys Val Phe Ser  
1 5 10 15

Ser Phe Ala Gln Ala Asn Asp Ser Lys Asn Gly Ala Phe Gly Met Ser  
20 25 30

Ala Gly Glu Lys Leu Leu Val Tyr Glu Thr Ser Lys Gln Asp Pro Ile  
35 40 45

Val Pro Phe Leu Leu Asn Leu Phe Leu Gly Phe Gly Ile Gly Ser Phe



50 55 60

Ala Gln Gly Asp Ile Leu Gly Gly Ser Leu Ile Leu Gly Phe Asp Ala  
65 70 75 80

Val Gly Ile Gly Leu Ile Leu Ala Gly Ala Tyr Leu Asp Ile Lys Ala  
85 90 95

Leu Asp Gly Ile Thr Lys Lys Ala Ala Phe Gln Trp Thr Trp Gly Lys  
100 105 110

Gly Val Met Leu Ala Gly Val Val Thr Met Ala Val Thr Arg Leu Thr  
115 120 125

Glu Ile Ile Leu Pro Phe Thr Phe Ala Asn Ser Tyr Asn Arg Lys Leu  
130 135 140

Lys Asn Ser Leu Asn Val Ala Leu Gly Gly Phe Glu Pro Ser Phe Asp  
145 150 155 160

Val Ala Met Gly Gln Ser Ser Ala Leu Gly Phe Glu Leu Ser Phe Lys  
165 170 175

Lys Ser Tyr  
179

## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia afzelii*
- (B) STRAIN: ACAI

## (ix) FEATURE:

DDETD " 23480560

(A) NAME/KEY: CDS  
(B) LOCATION: 219..755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GATTTTTCAT TGGATCCCAG AATTTGTAGA ATTTTCGACA AATAAAGACA TTATTAAAAG	60
AATTGAAATT GCTAATTTTA TGGTCAAATC AAGAAGCTCT ATTGGGAAGC GAATTTCAAG	120
TAATACTTTG AAAAAAGTTA AATTTAAATA GTTTTAAAAA CCTTTTAA ATTTCATTAA	180
TATGTTACTA TAATACCAGT TTTAATAAAG AGGTTTTT ATG AAT AAA TTT TTA	233
Met Asn Lys Phe <sup>2</sup> Leu	
1 5	
ATT GTT GTT TTG CTA GCC TTT TGT GTT TTT TCT AGC TTT GCT CAA GCT	281
Ile Val Val Leu Leu Ala Phe Cys Val Phe Ser Ser Phe Ala Gln Ala	
10 15 20	
GAT GAT TCT AAA AGC GCT TTT AAT TTG GGA GCG GGA GAA AAA CTT TTA	329
Asp Asp Ser Lys Ser Ala Phe Asn Leu Gly Ala Gly Glu Lys Leu Leu	
25 30 35	
GCT TAT GAA ACT AGT AAG AAA GAT CCT ATT GTG CCA TTT TTA TTG AAC	377
Ala Tyr Glu Thr Ser Lys Lys Asp Pro Ile Val Pro Phe Leu Leu Asn	
40 45 50	
CTT TTT TTA GGG TTT GGA ATA GGT TCT TTT GCT CAA GGA GAT ATT CTT	425
Leu Phe Leu Gly Phe Gly Ile Gly Ser Phe Ala Gln Gly Asp Ile Leu	
55 60 65	
GGG GGT TTT CTT ATT CTT GGA TTT GAT GCA GTT GGT ATA GGG TTA ATA	473
Gly Gly Phe Leu Ile Leu Gly Phe Asp Ala Val Gly Ile Gly Leu Ile	
70 75 80 85	
CTT ACA GGA GCT TAT TTA GAT ATC AAA GCT CTT GAT AAG AAT GCT CCA	521
Leu Thr Gly Ala Tyr Leu Asp Ile Lys Ala Leu Asp Lys Asn Ala Pro	
90 95 100	
AAA GCC GCT TTT AAG TGG ACT TGG GGT AAG GGA ATG ATG TTG GCA GGT	569
Lys Ala Ala Phe Lys Trp Thr Trp Gly Lys Gly Met Met Leu Ala Gly	
105 110 115	

DDB00487 28480560

GAAAATTAGA GCTTTTGTTT ATTATTTATA TTTTATTCT CTGCTAA 862

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 178 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Pro Phe Leu Leu Asn Leu Phe Leu Gly Phe Gly Ile Gly Ser Phe Ala

[illegible]

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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 749 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Borrelia garinii
    (B) STRAIN: IP90

(ix) FEATURE:
    (A) NAME/KEY: CDS
  
```

(B) LOCATION:192..725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TAGAATTTTC AACAAATAAA GATATTGTGA AAAGAATTGA AATTGCTAAT TTTATGGTTA	60
AATCAAGAAG CTCTATTGGT AAGCGAATTT CGAGTAACAA TTTGAAAAAA GTTAAATTTA	120
AATAGTTCCA AAAGCCTTTT TTAAATTTCA TTAATATGCT ACCATAATAC CAGTTTAATA	180
AAGGGGTTTT T ATG AAT AAG TTT TTA ATT TTT ATT TTG GTA ATC TTT TGT	230
Met Asn Lys Phe Leu Ile Phe Ile Leu Val Ile Phe Cys	
1 5 10	
GCT TTT TCT AGT TTT GCT CAA GAT GAT TCT AAA AGC ACT TTT AAT CTG	278
Ala Phe Ser Ser Phe Ala Gln Asp Asp Ser Lys Ser Thr Phe Asn Leu	
15 20 25	
GGA GCG GGA GAA AAA TTT TTG GTT TAT GAA ACT AAT AAG AAA GAT TCT	326
Gly Ala Gly Glu Lys Phe Leu Val Tyr Glu Thr Asn Lys Lys Asp Ser	
30 35 40 45	
CTT GTA CCA TTT TTA TTG AAC CTT TTT TTA GGG TTC GGG ATA GGT TCT	374
Leu Val Pro Phe Leu Leu Asn Leu Phe Leu Gly Phe Gly Ile Gly Ser	
50 55 60	
TTT GCT CAA GGA GAT ATC CTT GGA GGT TCT CTT ATT CTT GGA TTT GAT	422
Phe Ala Gln Gly Asp Ile Leu Gly Gly Ser Leu Ile Leu Gly Phe Asp	
65 70 75	
GCG GTT GGT ATA GGG TTA ATA CTT ACA GGA GCT TAT TTG GAC ATC AAG	470
Ala Val Gly Ile Gly Leu Ile Leu Thr Gly Ala Tyr Leu Asp Ile Lys	
80 85 90	
GAT TTT GAT AAT AAT GCT AAA AAA GCT GAT TTT AAG TGG ACT TGG GGT	518
Asp Phe Asp Asn Asn Ala Lys Lys Ala Asp Phe Lys Trp Thr Trp Gly	
95 100 105	
AAG GGA ATG ATG TTG GCA GGT GTG GTT ACT ATG GCT GTG ACA AGA TTG	566
Lys Gly Met Met Leu Ala Gly Val Val Thr Met Ala Val Thr Arg Leu	
110 115 120 125	

# SECRET

14

ACA GAA ATT GTT CTT CCA TTT ACA TTT GCT AAT AAT TAT AAC AGG AAG 614  
 Thr Glu Ile Val Leu Pro Phe Thr Phe Ala Asn Asn Tyr Asn Arg Lys  
 130 135 140

CTG AAA AAT AGT CTT AAT ATA GCC TTG GGA GGA TTT GAG CCT AGT TTT 662  
 Leu Lys Asn Ser Leu Asn Ile Ala Leu Gly Gly Phe Glu Pro Ser Phe  
 145 150 155

GAT ATT AAC ATG GGC CAA GCT AGT GCT CTT GGT TTT GGA CTG TCT TTC 710  
 Asp Ile Asn Met Gly Gln Ala Ser Ala Leu Gly Phe Gly Leu Ser Phe  
 160 165 170

AAA AAA AGC TAT TAA TTTTATTTAT CTAGAAAATG GGTG 749  
 Lys Lys Ser Tyr \*  
 175

## (2) INFORMATION FOR SEQ ID NO: 23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met Asn Lys Phe Leu Ile Phe Ile Leu Val Ile Phe Cys Ala Phe Ser  
 1 5 10 15

Ser Phe Ala Gln Asp Asp Ser Lys Ser Thr Phe Asn Leu Gly Ala Gly  
 20 25 30

Glu Lys Phe Leu Val Tyr Glu Thr Asn Lys Lys Asp Ser Leu Val Pro  
 35 40 45

Phe Leu Leu Asn Leu Phe Leu Gly Phe Gly Ile Gly Ser Phe Ala Gln  
 50 55 60

Gly Asp Ile Leu Gly Gly Ser Leu Ile Leu Gly Phe Asp Ala Val Gly  
 65 70 75 80

000120 28780550

(ii) MOLECULE TYPE: DNA (synthetic)

32

33

32

21



(2) INFORMATION FOR SEO ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TTGCTTACAG AATTCGCTGG GCGAAACGAA

30

(2) INFORMATION FOR SEO ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 109...396  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 30:

ACGAGCTCAA TCCAAACTTT ATTTGCTTGC AATAAATTAA TATTAATTTA TTATAAATTG 60  
CGCTAATATT TTA~~CTT~~GTCA AA~~ACT~~TACCA TTAGGAGATA ATAAAAAC ATG AAA AAA 117  
Met Lys Lys  
1

ATT TTC ACA TTA ATA TTA ATT TTT GGG TTG ACA ATT GAA ATC TTT GCC 165  
Ile Phe Thr Leu Ile Leu Ile Phe Gly Leu Thr Ile Glu Ile Phe Ala  
5 10 15

ACA AAA GAC ACA CAA AAT AGA ATT GAA AAA GGC ATT GAA AGT TTT AAC 213  
Thr Lys Asp Thr Gln Asn Arg Ile Glu Lys Gly Ile Glu Ser Phe Asn  
20 25 30 35

AAA TAT GAT AAA GAG AAA AAA AAT CCA ATA GGG CCA TTC CTT TTA AAT 261  
Lys Tyr Asp Lys Glu Lys Lys Asn Pro Ile Gly Pro Phe Leu Leu Asn  
40 45 50

TTA TTT TTG CCC TTT GGA ATA GGA TCC TTT GTC CAA GGG GAT TAT ATT 309  
Leu Phe Leu Pro Phe Gly Ile Gly Ser Phe Val Gln Gly Asp Tyr Ile

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55	60	65	
GGT GGA GGC TCA GTG CTT GGA TTT AAT TTA TTA GGA GCA ATC CTT TGG			357
Gly Gly Gly Ser Val Leu Gly Phe Asn Leu Leu Gly Ala Ile Leu Trp			
70	75	80	
GAA CTG GAA TTA TTC TTA ATC ACC GAG AAA CAC AAT TAA			396
Glu Leu Glu Leu Phe Leu Ile Thr Glu Lys His Asn			
85	90	95	

## (2) INFORMATION FOR SEQ ID NO: 31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met	Lys	Lys	Ile	Phe	Thr	Leu	Ile	Leu	Ile	Phe	Gly	Leu	Thr	Ile	Glu
1				5				10						15	
Ile	Phe	Ala	Thr	Lys	Asp	Thr	Gln	Asn	Arg	Ile	Glu	Lys	Gly	Ile	Glu
			20					25					30		
Ser	Phe	Asn	Lys	Tyr	Asp	Lys	Glu	Lys	Lys	Asn	Pro	Ile	Gly	Pro	Phe
		35					40					45			
Leu	Leu	Asn	Leu	Phe	Leu	Pro	Phe	Gly	Ile	Gly	Ser	Phe	Val	Gln	Gly
	50					55				60					
Asp	Tyr	Ile	Gly	Gly	Gly	Ser	Val	Leu	Gly	Phe	Asn	Leu	Leu	Gly	Ala
65					70					75				80	
Ile	Leu	Trp	Glu	Leu	Glu	Leu	Phe	Leu	Ile	Thr	Glu	Lys	His	Asn	
				85					90				95		

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